

RESULT 1

US-08-252-384C-2

; Sequence 2, Application US/08252384C

; GENERAL INFORMATION:

; APPLICANT: Reactive Surfaces, Ltd.

; APPLICANT: McDaniel, Steven

; APPLICANT: Raushel, Frank M

; APPLICANT: Wild, James R

; TITLE OF INVENTION: Recombinant Organophosphorous Acid Anhydrase and Methods of Use

; FILE REFERENCE: TAMK145

; CURRENT APPLICATION NUMBER: US/08/252,384C

; CURRENT FILING DATE: 1994-06-01

; PRIOR APPLICATION NUMBER: US 07/928,540

; PRIOR FILING DATE: 1992-08-13

; PRIOR APPLICATION NUMBER: US 07/344,258

; PRIOR FILING DATE: 1989-04-27

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2

; LENGTH: 365

; TYPE: PRT

; ORGANISM: Pseudomonas diminuta

US-08-252-384C-2

Query Match 100.0%; Score 1831; DB 4; Length 365;

Best Local Similarity 100.0%; Pred. No. 3.5e-170;

Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	121	DVHIVAATGLWFDPPPLSMRLRSVEELTQFFLREIQYGIEDTGIRAGIIKV	ATTGKATPFQ	180
Qy	181	ELVLKAAARASLATGVPVTHTTAASQRDGEQQAAIFESEGLSPSRVCIGH	SDDTDDL	240
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Db	241	TALAARGYLIGLDHIPHSAIGLEDNASASALLGIRSWQTRALLIKALIDQ	GYMKQIL	300
Qy	301	DWLFGFSSYVTNIMDVMDRVNPDGMAFIPLRVI PFLREKGV	PQETLAGITVTN	360
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RESULT 8

US-08-252-384B-2

; Sequence 2, Application US/08252384B

; GENERAL INFORMATION:

; APPLICANT: Reactive Surfaces, Ltd.

; TITLE OF INVENTION: Recombinant Organophosphorus Acid Anhydrase and Methods of Use

; FILE REFERENCE: RACT-00100

; CURRENT APPLICATION NUMBER: US/08/252,384B

; CURRENT FILING DATE: 1994-06-01

; PRIOR APPLICATION NUMBER: 07/928,540

; PRIOR FILING DATE: 1992-08-13

; PRIOR APPLICATION NUMBER: 08/252,384

; PRIOR FILING DATE: 1994-06-01

; PRIOR APPLICATION NUMBER: 07/344,258

; PRIOR FILING DATE: 1989-04-27

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2

; LENGTH: 337

; TYPE: PRT

; ORGANISM: Pseudomonas diminuta

US-08-252-384B-2

Query Match 90.3%; Score 1653; DB 12; Length 337;

Best Local Similarity 99.7%; Pred. No. 3.3e-112;

Matches 327; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db	62	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHIVAATGLWFDPLSMRLRSVEELTQF	121
Qy	150	FLREIQYGIEDTGIRAGIIKVATT	GKATPFQELVLKAAARASLATGVPVTTHTAASQRDG	209
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Qy	210	EQQAAlFESEGLSPSRVCIGHSD	DDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS	269
Db	182	EQQAAlFESEGLSPSRVCIGHSD	DDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS	241
Qy	270	ALLGIRSWQTRALLIKALIDQGY	MKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP	329
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RESULT 4

US-08-252-384A-1

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; Sequence 1, Application US/08252384A
; GENERAL INFORMATION:
; APPLICANT: Reactive Surfaces
; APPLICANT: McDaniel, C. Steven
; TITLE OF INVENTION: Recombinant Organophosphorus Acid Anhydrase and Methods
of Use
; FILE REFERENCE: RACT-00200
; CURRENT APPLICATION NUMBER: US/08/252,384A
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: 07/928,540
; PRIOR FILING DATE: 1992-08-13
; PRIOR APPLICATION NUMBER: 08/252,384
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 07/344,258
; PRIOR FILING DATE: 1989-04-27
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-08-252-384A-1
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Best Local Similarity 100.0%; Pred. No. 3.9e-115;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

5484728-2

;Patent No. 5484728

; APPLICANT: SEERDAR, CUNEYT M.;MURDOCK, DOUGLAS

; TITLE OF INVENTION: PARATHION HYDROLASE ANALOGS AND METHODS

;FOR PRODUCTION AND PURIFICATION

; NUMBER OF SEQUENCES: 6

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/333, 8892

; FILING DATE: 01-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 898,973

; FILING DATE: 25-JUN-1992

; APPLICATION NUMBER: 312,503

; FILING DATE: 17-FEB-1989

; APPLICATION NUMBER: 237,255

; FILING DATE: 26-AUG-1988

;SEQ ID NO:2:

; LENGTH: 365

5484728-2

Query Match 99.4%; Score 1688; DB 6; Length 365;

Best Local Similarity 99.7%; Pred. No. 6.9e-174;

Matches 335; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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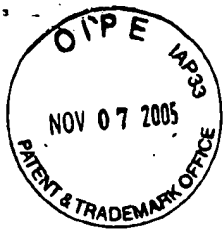
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in patent #10 (N)



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McDaniel, Steven
Raushel, Frank M
Wild, James R

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<130> TAMK145

<140> US 08/252,384
<141> 1994-06-01

<150> US 07/928,540
<151> 1992-08-13

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RACT-00100.ST25

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SEQUENCE LISTING

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- <120> Recombinant Organophosphorus Acid Anhydrase and Methods of Use
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- <140> US 08/252,384 A
- <141> 2004-06-01
- <150> 07/928,540
- <151> 1992-08-13
- <150> 08/252,384
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gtg gcg gcg acc ggc ttg tgg ttc gac ccg cca ctt tcg atg cga ttg      336
Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu
100          105          110

agg agt gta gag gaa ctc aca cag ttc ttc ctg cgt gag att caa tat      384
Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr

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115	120	125	
ggc atc gaa gac acc gga att agg gcg ggc att atc aag gtc gcg acc Gly Ile Glu Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr 130 135 140			432
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cgg gcc agc ttg gcc acc ggt gtt ccg gta acc act cac acg gca gca Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala 165 170 175			528
agt cag cgc gat ggt gag cag cag gcc gcc att ttt gag tcc gaa ggc Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly 180 185 190			576
ttg agc ccc tca cgg gtt tgt att ggt cac agc gat gat act gac gat Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp 195 200 205			624
ttg agc tat ctc acc gcc ctc gct gcg cgc gga tac ctc atc ggt cta Leu Ser Tyr Leu Thr Ala Leu Ala Arg Gly Tyr Leu Ile Gly Leu 210 215 220			672
gac cac atc ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala 225 230 235 240			720
tca gcc ctc ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile 245 250 255			768
aag gcg ctc atc gac caa ggc tac atg aaa caa atc ctc gtt tcg aat Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn 260 265 270			816
gac tgg ctg ttc ggg ttt tcg agc tat gtc acc aac atc atg gac gtg Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val 275 280 285			864
atg gat cgc gtg aac ccc gac ggg atg gcc ttc att cca ctg aga gtg Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val 290 295 300			912
atc cca ttc gta cga gag aag ggc gtc cca cag gaa acg ctg gca ggc Ile Pro Phe Val Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly 305 310 315 320			960
atc act gtg act aac ccg gcg cgg ttc tat gtc acc gac ctt gcg ggc Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly 325 330 335			1008
gtc atg Val			1014

<210> 2
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 <212> PRT
 <213> Pseudomonas diminuta

<400> 2

Met Ser Ile Gly Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile
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Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly
20 25 30

Ser Ser Ala Gly Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg
35 40 45

Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala
50 55 60

Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg
65 70 75 80

Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile
85 90 95

Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu
100 105 110

Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr
115 120 125

Gly Ile Glu Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr
130 135 140

Thr Gly Lys Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala
145 150 155 160

Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala
165 170 175

Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly
180 185 190

Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp
195 200 205

Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu
210 215 220

Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala
225 230 235 240

Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile
245 250 255

Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn
260 265 270

Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val
275 280 285

Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val
290 295 300

Ile Pro Phe Val Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly
305 310 315 320

Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly
325 330 335

Val



Organization Applicant RACT00200 2nd Amd Seq Listing.WorkFile

Street :
City :
State :
Country :
PostalCode :
PhoneNumber :
FaxNumber :
EmailAddress :

<110> OrganizationName : Reactive Surfaces, Ltd.

Application Project

<120> Title : Recombinant Organophosphorus Acid Anhydrase and Methods of Use
<130> AppFileReference : RACT-00200
<140> CurrentAppNumber : Unknown
<141> CurrentFilingDate : 2003-01-02

Earlier Applications

<150> PriorAppNumber : 07/928,540
<151> PriorFilingDate : 1992-08-13

Earlier Applications

<150> PriorAppNumber : 08/252,384
<151> PriorFilingDate : 1994-06-01

Earlier Applications

<150> PriorAppNumber : 07/344,258
<151> PriorFilingDate : 1989-04-27

Sequence

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tggccagagt tcttcggtag ccgcaaagct ctagcggaaa aggctgtgag aggattgcgc 180
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gacgtcagtt tattggccga ggtttcgcgg gctgcccagc ttcatatcgt ggccggcgacc 300
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ttcttctctg gtgagattca atatggcatc gaagacaccg gaattagggc gggcattatc 420
aaggctcgcga ccacaggcaa ggcgaccccc ttccaggagt tagtgtaaa ggcggccgcc 480
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ctcatcggtc tagaccacat cccgcacagt gcgattggtc tagaagataa tgcgagtgca 720
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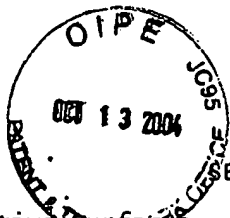
RACT00200 2nd Amd Seq Listing.WorkFile

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ccactgagag tgatcccatt cgtacgagag aagggcggtc cacaggaaac gctggcaggc	960
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SequenceDescription :

Feature

Sequence: RACT00200 Amd Seq:
<221> FeatureKey : CDS
<222> LocationFrom : 1
<222> LocationTo : 1011
Other Information :
CDSJoin : No



RACT00200 Sequence Listing
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<110> Reactive Surfaces
McDaniel, C. Steven

<120> Recombinant Organophosphorus Acid Anhydrase and Methods of Use

<130> RACT-00200

<140> Unknown

<141> 2002-12-23

<150> 07/928,540

<151> 1992-08-13

<150> 08/252,384

<151> 1994-06-01

<150> 07/344,258

<151> 1989-04-27

<160> 1

<170> PatentIn version 3.2

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<211> 337

<212> PRT

<213> Pseudomonas aeruginosa

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35 40 45

Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala
50 55 60

Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg
65 70 75 80

Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile
85 90 95

Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu
100 105 110

Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr
115 120 125

RACT00200 Sequence Listing

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Thr Gly Lys Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala
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Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala
165 170 175

Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly
180 185 190

Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp
195 200 205

Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu
210 215 220

Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala
225 230 235 240

Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile
245 250 255

Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn
260 265 270

Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val
275 280 285



Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val
290 295 300

Ile Pro Phe Leu Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly
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Ile Thr Val Thr Asn Pro Ala Arg Phe Leu Ser Pro Thr Leu Arg Ala
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Ser

SEQUENCE LISTING



<110> Reactive Surfaces
McDaniel, C. Steven
<120> Recombinant Organophosphorus Acid Anhydrase and Methods of Use
<130> RACT-00200
<140> Unknown
<141> 2002-12-28
<150> 07/928,540
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35 40 45
Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala
50 55 60

E3
CONF

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Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile
85 90 95

Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu
100 105 110

Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr
115 120 125

Gly Ile Glu Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr
130 135 140

Thr Gly Lys Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala
145 150 155 160

Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala
165 170 175

Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly
180 185 190

Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp
195 200 205

Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu
210 215 220

Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala
225 230 235 240

Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile
245 250 255

Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn
260 265 270

Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val
275 280 285

Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val
290 295 300

Ile Pro Phe Leu Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly
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Ile Thr Val Thr Asn Pro Ala Arg Phe Leu Ser Pro Thr Leu Arg Ala
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Ser

SEQUENCE LISTING

<110> Reactive Surfaces, Ltd.

<120> Recombinant Organophosphorus Acid Anhydrase and Methods of Use

<130> RACT-00200

<140> Unknown

<141> 2003-01-02

<150> 07/928,540

<151> 1992-08-13

<150> 08/252,384

<151> 1994-06-01

<150> 07/344,258

<151> 1989-04-27

<160> 2

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5

10

15

aca atc tct gaa gcg ggt ttc aca ctg act cac gag cac atc tgc ggc

96

Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly

20

25

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agc tcg gca gga ttc ttg cgt gct tgg cca gag ttc ttc ggt agc cgc
144
Ser Ser Ala Gly Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg

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40

45

aaa gct cta gcg gaa aag gct gtg aga gga ttg cgc cgc gcc aga gcg
192
Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala

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55

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240
Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg

65

70

75

80

gac gtc agt tta ttg gcc gag gtt tcg cgg gct gcc gac gtt cat atc
288
Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile

85

90

95

gtg gag gcg acc ggc ttg tgg ttc gac ccg cca ctt tcg atg cga ttg
336
Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu

100

105

110

agg agt gta gag gaa ctc aca cag ttc ttc ctg cgt gag att caa tat
384
Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr

115

120

125

ggc atc gaa gac acc gga att agg gcg ggc att atc aag gtc gcg acc
432
Gly Ile Glu Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr

130 135 140

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480
Thr Gly Lys Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala

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528
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576
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624
Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp

195 200 205

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672
Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu

210 215 220

gac cac atc ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca
720
Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala

225 230 235 240

tca gcc ctc ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc
768

Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile

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250

255

aag gcg ctc atc gac caa ggc tac atg aaa caa atc ctc gtt tog aat

816

Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn

260

265

270

gac tgg ctg ttc ggg ttt tog agc tat gtc acc aac atc atg gac gtg

864

Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val

275

280

285

atg gat cgc gtg aac ccc gac ggg atg gcc ttc att cca ctg aga gtg

912

Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val

290

295

300

atc cca ttc gta cga gag aag ggc gtc cca cag gaa acg ctg gca ggc

960

Ile Pro Phe Val Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly

305

310

315

320

atc act gtg act aac ccg gcg cgg ttc tat gtc acc gac ctt gcg ggc

1008

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gtc atg

1014

Val

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<212> PRT
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20 25 30

Ser Ser Ala Gly Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg
35 40 45

Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala
50 55 60

Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg
65 70 75 80

Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile
85 90 95

Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu
100 105 110

Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr
115 120 125

Gly Ile Glu Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr
130 135 140

Thr Gly Lys Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala
145 150 155 160

Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala

165

170

175

Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly
180 185 190

Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp
195 200 205

Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu
210 215 220

Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala
225 230 235 240

Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile
245 250 255

Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn
260 265 270

Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val
275 280 285

Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val
290 295 300

Ile Pro Phe (Val) Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly
305 310 315 320

Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly
325 330 335

Val

Protein Comparisons Percent Identity

McDaniel vs Wild Lab 57.8%
McDaniel vs Serdar 59.5%
Serdar vs Wild Lab 100%

DNA Comparisons Percent Identity

McDaniel vs Wild Lab 88.0%
McDaniel vs Serdar 83.7%
Serdar vs Wild Lab 99.6%

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Wild Lab.PRO Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Arg Thr Leu Leu Gly Gly Leu Ala Gly Cys Ala Thr Trp Leu Asp Arg 2
Serdar.pro Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Arg Thr Leu Leu Gly Gly Leu Ala Gly Cys Ala Thr Trp Leu Asp Arg 30

McDaniel.pro Ser Ala Gln Ala Met Arg Ser Ile Arg Ala Arg Pro Ile Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu Asp Ile Ser Ala 58
Wild Lab.PRO Ser Ala Gln Ala Met Arg Ser Ile Arg Ala Arg Pro Ile Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu Asp Ile Ser Ala 58
Serdar.pro Ser Ala Gln Ala Met Arg Ser Ile Arg Ala Arg Pro Ile Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu Asp Ile Ser Ala 60

McDaniel.pro Ala Arg Gln Asp Ser Cys Val Leu Gly Gln Ser Ser Ser Val Ala Gln Ser Ser Ser Gly Lys Gly Cys Glu Arg 83
Wild Lab.PRO Ala Arg Gln Asp Ser Cys Val Leu Gly Gln Ser Ser Ser Val Ala Gln Ser Ser Ser Gly Lys Gly Cys Glu Arg 83
Serdar.pro Ala Arg Gln Asp Ser Cys Val Leu Gly Gln Ser Ser Ser Val Ala Gln Ser Ser Ser Gly Lys Gly Cys Glu Arg 88

McDaniel.pro Ile Ala Arg Gln Ser Gly Trp Arg Ala Asn Asp Cys Arg Cys Val Asp Phe Arg Tyr Arg Ser Arg Arg Gln Phe Ile Gly Arg Gly Phe 11
Wild Lab.PRO Ile Ala Arg Gln Ser Gly Trp Arg Ala Asn Asp Cys Arg Cys Val Asp Phe Arg Tyr Arg Ser Arg Arg Gln Phe Ile Gly Arg Gly Phe 11
Serdar.pro Ile Ala Arg Gln Ser Gly Trp Arg Ala Asn Asp Cys Arg Cys Val Asp Phe Arg Tyr Arg Ser Arg Arg Gln Phe Ile Gly Arg Gly Phe 11

McDaniel.pro Ala Gly Cys Arg Arg Ser Tyr Leu Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Tyr Val Glu Glu Leu Thr 14
Wild Lab.PRO Ala Gly Cys Arg Arg Ser Tyr Leu Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Tyr Val Glu Glu Leu Thr 14
Serdar.pro Ala Gly Cys Arg Arg Ser Tyr Leu Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Tyr Val Glu Glu Leu Thr 14

McDaniel.pro Leu Val Leu Pro Ala Val Arg Phe Asn Met Ala Ser Lys Tyr Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys 17
Wild Lab.PRO Leu Val Leu Pro Ala Val Arg Phe Asn Met Ala Ser Lys Tyr Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys 17
Serdar.pro Leu Val Leu Pro Ala Val Arg Phe Asn Met Ala Ser Lys Tyr Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys 17

McDaniel.pro Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20
Wild Lab.PRO Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20
Serdar.pro Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20

McDaniel.pro Gln Arg Asp Gly Glu Arg Gly Arg Pro Pro Phe Leu Ser Pro Lys Leu Glu Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp 23
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Wild Lab.PRO Asp Leu Ser Tyr Leu Thr Ala Leu Leu Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn 26
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McDaniel.pro Ala Ser Ala Ser Pro Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln 29
Wild Lab.PRO Ala Ser Ala Ser Pro Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln 29
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McDaniel.pro Ile Leu Val Ser Asn Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val Asn Pro Asp Gly Met 32
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Serdar.pro Ile Leu Val Ser Asn Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val Asn Pro Asp Gly Met 32

McDaniel.pro Ala Phe Ile His 32
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Serdar.pro Ala Phe Ile His 32

McDaniel.pro Arg Phe Leu Ser Pro Thr Leu Arg Ala Ser 32
Wild Lab.PRO Arg Phe Leu Ser Pro Thr Leu Arg Ala Ser 32
Serdar.pro Arg Phe Leu Ser Pro Thr Leu Arg Ala Ser 36

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Decoration 'Decoration #1': Shade (with black at 10% fill) residues that differ from McDaniel.pro.

Decoration 'Decoration #2': Box residues that differ from McDaniel.pro.

1 A T G C A A A C G A G A A G G G T T G T G C T C / C T C G C G C C G C G C - - - G A G A A C T C T McDaniel P diminu
2 A T G C A A A C G A G A A G G G T T G T G C T C / C T C G C G C C G C G C - - - G A G A A C T C T Wild lab opd...seq
3 A T G C A A A C G A G A A G G G T T G T G C T C / C T C G C G C C G C G C - - - G A G A A C T C T Serdar, seq

48 G U T C G C G C G C C T G G C T G G T G C G C G A - C G T G C G T C G A T C G A T C G C C A C A G McDaniel P diminu
4 G U T C G C G C G C C T G G C T G G T G C G C G A - C G T G C G T C G A T C G A T C G C C A C A G Wild lab opd, seq
53 G U T C G C G C G C C T G G C T G G T G C G C G A - C G T G C G T C G A T C G A T C G C C A C A G Serdar, seq

97 G C C A T C C G A T C A A T A C - G T G C G C G - T C C T A T C A C A A T C T C G A A G C G G T McDaniel P diminu
97 G C C A T C C G A T C A A T A C - G T G C G C G - T C C T A T C A C A A T C T C G A A G C G G T Wild lab opd, seq
101 G C C A T C C G A T C A A T A C - G T G C G C G - T C C T A T C A C A A T C T C G A A G C G G T Serdar, seq

145 T T C A C A G T G A C T C A C C A G A C A T C T - G G C A G C T C G G C A C G A T T C T G C G McDaniel P diminu
145 T T C A C A G T G A C T C A C C A G A C A T C T - G G C A G C T C G G C A C G A T T C T G C G Wild lab opd, seq
151 T T C A C A G T G A C T C A C C A G A C A T C T - G G C A G C T C G G C A C G A T T C T G C G Serdar, seq

194 T G C T T G G C C A G A G T T C T T C G G T A G C - C A A A A G C T C T A G C G A A A A G C C T G McDaniel P diminu
194 T G C T T G G C C A G A G T T C T T C G G T A G C - C A A A A G C T C T A G C G A A A A G C C T G Wild lab opd, seq
201 T G C T T G G C C A G A G T T C T T C G G T A G C - C A A A A G C T C T A G C G A A A A G C C T G Serdar, seq

243 T G A C A G G A T T G C G C - - - G C C A G A G C G G C T G C G T G C C A A C C A T T G T C G A T McDaniel P diminu
243 T G A C A G G A T T G C G C - - - G C C A G A G C G G C T G C G T G C C A A C C A T T G T C G A T Wild lab opd, seq
251 T G A C A G G A T T G C G C - - - G C C A G A G C G G C T G C G T G C C A A C C A T T G T C G A T Serdar, seq

290 G T C T G C A C T T T C C A T A T C G G T C G C C A C G T C A G T T T A T T G G C C C A G G T T T C McDaniel P diminu
290 G T C T G C A C T T T C C A T A T C G G T C G C C A C G T C A G T T T A T T G G C C C A G G T T T C Wild lab opd, seq
301 G T C T G C A C T T T C C A T A T C G G T C G C C A C G T C A G T T T A T T G G C C C A G G T T T C Serdar, seq

340 G U G G C C T G C C G A A G T T C A T A T C - T G G C G C C A C G C G C C T T G C G T T G G A C C McDaniel P diminu
340 G U G G C C T G C C G A A G T T C A T A T C - T G G C G C C A C G C G C C T T G C G T T G G A C C Wild lab opd, seq
351 G U G G C C T G C C G A A G T T C A T A T C - T G G C G C C A C G C G C C T T G C G T T G G A C C Serdar, seq

380 C C C C A C T T T C G A T C C A T T G A C C T A T G T A G G A A C T C A C A C T A G T T C T T McDaniel P diminu
380 C C C C A C T T T C G A T C C A T T G A C C T A T G T A G G A A C T C A C A C T A G T T C T T Wild lab opd, seq
401 C C C C A C T T T C G A T C C A T T G A C C T A T G T A G G A A C T C A C A C T A G T T C T T Serdar, seq

439 C C T G C G T T G A G A T T C A A T A T G C A T C G A A G T A C A C C G G A A T T A G G G C G C G McDaniel P diminu
439 C C T G C G T T G A G A T T C A A T A T G C A T C G A A G T A C A C C G G A A T T A G G G C G C G Wild lab opd, seq
450 C C T G C G T T G A G A T T C A A T A T G C A T C G A A G T A C A C C G G A A T T A G G G C G C G Serdar, seq

480 C A T T A T C A A G G T C C G A C C A A G G C A A G G C A C C C C C T T T C A G G A G T T A G McDaniel P diminu
480 C A T T A T C A A G G T C C G A C C A A G G C A A G G C A C C C C C T T T C A G G A G T T A G Wild lab opd, seq
498 C A T T A T C A A G G T C C G A C C A A G G C A A G G C A C C C C C T T T C A G G A G T T A G Serdar, seq

538 T G T T A A A G C G G C C C C C G G G C A G C T T G C C A C G G T G T T C C G G T A A C C McDaniel P diminu
538 T G T T A A A G C G G C C C C C G G G C A G C T T G C C A C G G T G T T C C G G T A A C C Wild lab opd, seq
548 T G T T A A A G C G G C C C C C G G G C A G C T T G C C A C G G T G T T C C G G T A A C C Serdar, seq

588 A C T C A C A C C C C A G C A A G T C A G C G C G A T C G T G A C C G A G C A G C C C C C A T T McDaniel P diminu
588 A C T C A C A C C C C A G C A A G T C A G C G C G A T C G T G A C C G A G C A G C C C C C A T T Wild lab opd, seq
594 A C T C A C A C C C C A G C A A G T C A G C G C G A T C G T G A C C G A G C A G C C C C C A T T Serdar, seq

628 T T T G A G T C C G A A G - G T T G A G C C G - T G A C C G G T T T G T A T T G G T C A C A C C G A McDaniel P diminu
628 T T T G A G T C C G A A G - G T T G A G C C G - T G A C C G G T T T G T A T T G G T C A C A C C G A Wild lab opd, seq
646 T T T G A G T C C G A A G - G T T G A G C C G - T G A C C G G T T T G T A T T G G T C A C A C C G A Serdar, seq

682 T G A T A C T G A C G A T T T G A G C T A T C T A C C G C C G T - G C T C G C G C - - G A T A C G McDaniel P diminu
682 T G A T A C T G A C G A T T T G A G C T A T C T A C C G C C G T - G C T C G C G C - - G A T A C G Wild lab opd, seq
696 T G A T A C T G A C G A T T T G A G C T A T C T A C C G C C G T - G C T C G C G C - - G A T A C G Serdar, seq

734 T C A T C G G T C T A G A C C A C A T C C C G C C A C A G T G C G A T T G G T C T A G A A G A T A A T McDaniel P diminu
734 T C A T C G G T C T A G A C C A C A T C C C G C C A C A G T G C G A T T G G T C T A G A A G A T A A T Wild lab opd, seq
748 T C A T C G G T C T A G A C C A C A T C C C G C C A C A G T G C G A T T G G T C T A G A A G A T A A T Serdar, seq

784 G C G A G T G C A T C A C C G C T C C T G G G C A T C C G T T C G T G C A A A C A C G G G T C T McDaniel P diminu
784 G C G A G T G C A T C A C C G C T C C T G G G C A T C C G T T C G T G C A A A C A C G G G T C T Wild lab opd, seq
796 G C G A G T G C A T C A C C G C T C C T G G G C A T C C G T T C G T G C A A A C A C G G G T C T Serdar, seq

834 C T T G A T C A A G G C C C T C A T C G A C C A A G G C T A G A T G A A A C A A A T C C T C G T T T McDaniel P diminu
834 C T T G A T C A A G G C C C T C A T C G A C C A A G G C T A G A T G A A A C A A A T C C T C G T T T Wild lab opd, seq
848 C T T G A T C A A G G C C C T C A T C G A C C A A G G C T A G A T G A A A C A A A T C C T C G T T T Serdar, seq

884 C G A A T G A C T G C C T G T T G G G T T T G G A G C T A T G C C A A C A T C A T G A C McDaniel P diminu
884 C G A A T G A C T G C C T G T T G G G T T T G G A G C T A T G C C A A C A T C A T G A C Wild lab opd, seq
896 C G A A T G A C T G C C T G T T G G G T T T G G A G C T A T G C C A A C A T C A T G A C Serdar, seq

934 G T A T G G A T C C C C T C A A C C C C A C G G A T G C C T T C A T T C - A C T G A G A G T McDaniel P diminu
934 G T A T G G A T C C C C T C A A C C C C A C G G A T G C C T T C A T T C - A C T G A G A G T Wild lab opd, seq
946 G T A T G G A T C C C C T C A A C C C C A C G G A T G C C T T C A T T C - A C T G A G A G T Serdar, seq

984 G A T C C C A T T C - T A C C A G A G A A G G C C T C C C A C A G G A A A C G C T G C A G G C A McDaniel P diminu
984 G A T C C C A T T C - T A C C A G A G A A G G C C T C C C A C A G G A A A C G C T G C A G G C A Wild lab opd, seq
996 G A T C C C A T T C - T A C C A G A G A A G G C C T C C C A C A G G A A A C G C T G C A G G C A Serdar, seq

1032 T C A C T G T C A T A A C C C G C C G G T T C T G T C A C C G A C T T G C C C T G C - - - McDaniel P diminu
1032 T C A C T G T C A T A A C C C G C C G G T T C T G T C A C C G A C T T G C C C T G C - - - Wild lab opd, seq
1046 T C A C T G T C A T A A C C C G C C G G T T C T G T C A C C G A C T T G C C C T G C - - - Serdar, seq

1079 A T G A McDaniel P diminu
1011 A T G A Wild lab opd, seq
1085 A T G A Serdar, seq

Decorations 'Decorations VI': Spade (with black on 100 (11)) residues that differ from McDonald P diminuta, spq.

Decorations 'Decorations 02': No residues that differ from McDaniel & diminuta.ssp.

Works Cited

McDaniel P. diminuta :

McDaniel, C.S., Harper, L.L. and Wild, J.R., Cloning and sequencing of a plasmid-borne gene (opd) encoding a phosphotriesterase, J. Bacteriol. 170 (5), 2306-2311 (1988). Gene Bank Accession Number: M20392

Oph-lab RC: Wild lab DNA sequence

Serdar: Serdar Sequence obtained from United States Patent and Trademark Office (uspto.gov) Patent Number 5,484,728

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FILED 12-23-02 AND 01-02-03.

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						
No.	Score	Match	Length	DB	ID	Description		
1	1693	99.7	365	2	A43720	parathion hydrolas		
2	913	53.8	325	2	A28214	phosphotriesterase		
3	448	26.4	326	2	D70962	hypothetical prote		
4	408	24.0	314	2	F90424	hypothetical prote		
5	385	22.7	323	2	E75459	probable phosphotr		
6	331	19.5	305	2	AB1321	probable phosphotr		
7	309	18.2	331	2	A83678	hypothetical prote		
8	308	18.1	292	2	F65132	hypothetical 32.9		
9	296	17.4	679	2	F83723	hypothetical prote		
10	277.5	16.3	355	2	AD2933	hypothetical prote		
11	277.5	16.3	355	2	C98349	resiniferatoxin-bi		
12	273	16.1	344	2	AC0994	puative phophotrie		
13	269.5	15.9	330	2	AG1405	Phosphotriesterase		
14	268.5	15.8	330	2	AG1781	Phosphotriesterase		
15	229	13.5	351	2	A99586	conserved hypothet		

RESULT 1

A43720

parathion hydrolase precursor - *Flavobacterium* sp. (ATCC 27551)

C;Species: *Flavobacterium* sp.

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 08-Oct-1999

C;Accession: A43720

R;Mulbry, W.W.; Kams, J.S.

J. Bacteriol. 171, 6740-6746, 1989

A;Title: Parathion hydrolase specified by the *Flavobacterium* opd gene: relationship between the gene and protein.

A;Reference number: A43720; MUID:90078122; PMID:2556372

A;Accession: A43720

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-365 <MUL>

A;Cross-references: GB:M29593; NID:g148712; PIDN:AAA24930.1; PID:g148713

A;Experimental source: ATCC 27551

Query Match 99.7%; Score 1693; DB 2; Length 365;

Best Local Similarity 100.0%; Pred. No. 1.1e-126;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2

SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR
61

|||||

Db 30

SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR
89

Qy 62

ARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHIVAATGLWFDPPLSMRLRSVEELTQF
121

|||||

Db 90

ARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHIVAATGLWFDPPLSMRLRSVEELTQF
149

Qy 122

FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG

181

|||||

Db 150

FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG

209

Qy 182

EQQAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS

241

|||||

Db 210

EQQAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS

269

Qy 242

ALLGIRSWQTRALLIKALIDQGYMKQILVSNWDLFGFSSYVTNIMDVMDRVNPDGMAFIP

301

|||||

Db 270

ALLGIRSWQTRALLIKALIDQGYMKQILVSNWDLFGFSSYVTNIMDVMDRVNPDGMAFIP

329

Qy 302 LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 337

|||||

Db 330 LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 365

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		Query		DB	ID	Description
		Match	Length	Match	Length			
1	1695	99.8	337	5	ABB79958			Abb79958 Organopho
2	1693	99.7	336	6	ABG72651			Abg72651 Flavobact
3	1693	99.7	365	2	AAR05573			Aar05573 Parathion
4	1693	99.7	365	6	ABB82802			Abb82802 Flavobact
5	1689	99.5	336	6	ABG72650			Abg72650 Flavobact
6	1686	99.3	357	2	AAy43487			Aay43487 Amino aci
7	1685	99.2	334	2	AAy43486			Aay43486 Amino aci
8	1558	91.8	356	6	ABB82799			Abb82799 A. radiob
9	1558	91.8	384	6	ABB82798			Abb82798 A. radiob
10	1552	91.4	384	6	ABB82801			Abb82801 A. radiob
11	1535	90.4	384	6	ABB82800			Abb82800 A. radiob
12	465	27.4	326	6	ABU33918			Abu33918 Protein e
13	448	26.4	326	6	ABU36432			Abu36432 Protein e
14	400	23.6	306	6	ABU34486			Abu34486 Protein e
15	372.5	21.9	346	6	ABU31613			Abu31613 Protein e
16	331	19.5	305	5	ABB48499			Abb48499 Listeria
17	331	19.5	305	6	ABU32460			Abu32460 Protein e
18	308	18.1	292	6	ABU14978			Abu14978 Protein e
19	283	16.7	345	6	ABU21704			Abu21704 Protein e
20	273	16.1	344	6	ABU47684			Abu47684 Protein e
21	273	16.1	344	6	ABU47288			Abu47288 Protein e
22	269.5	15.9	330	5	ABB47719			

RESULT 1

ABB79958

ID ABB79958 standard; protein; 337 AA.

XX

AC ABB79958;

XX

DT 12-DEC-2002 (first entry)

XX

DE Organophosphorous hydrolase.

XX

KW Organophosphorous hydrolase; OPH; enzyme; immobilisation;

KW chemical warfare; pesticide; pollutant; detoxification; decontamination.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Peptide 1. .29

FT /label= Signal_peptide

FT Protein 30. .337

FT /label= Mature_protein

XX

PN WO200268454-A2.

XX

PD 06-SEP-2002.

XX

PF 21-FEB-2002; 2002WO-US005755.

XX

PR 21-FEB-2001; 2001US-00791138.

PR 20-FEB-2002; 2002US-00081737.

XX

PA (BATT) BATTELLE MEMORIAL INST.

XX

PI Ackerman EJ, Liu J, Chenghong L;

XX

DR WPI; 2002-713364/77.

DR N-PSDB; ABQ81428.

XX

PT Protein system, for facilitating chemical reactions e.g. hydrolysis,

PT oxidation, hydrogenation and proteolysis, comprises porous matrix

PT material and protein within matrix.

XX

PS Example; Fig 4; 56pp; English.

XX

CC The present sequence is the protein sequence of an organophosphorous
 CC hydrolase (OPH) encoded by an expression plasmid of the invention. The
 CC invention provides a method for producing OPH by transfecting a host cell
 CC with a vector comprising a sequence encoding OPH linked to a T7
 CC expression control sequence, culturing the transfected host cell, and
 CC purifying OPH from the cell or culture medium. This OPH has an activity
 CC of about 13,000 U/mg. The host cell can be prokaryotic, e.g. Escherichia
 CC coli, or eukaryotic, e.g. Pichia pastoris. The invention also provides a
 CC protein system for facilitating chemical reactions. The protein system
 CC comprises a porous matrix material having a pore volume of which at least
 CC 90% is composed of pores of 50-400 Angstroms. The protein occupies 5-40%
 CC of the average pore volume, and is preferably an enzyme, especially OPH
 CC having an activity of 60-95% that of the active state and retaining about
 CC 10% of its activity after 24 hr under alkaline conditions. The porous

CC matrix may comprise surface hydroxyls that are reacted with a coupling
 CC agent to form a functionalised monolayer. The system provides high enzyme
 CC activities on a porous support, stability under a variety of conditions,
 CC high densities of active protein and capability in industrial-scale
 CC applications. It provides environmentally safe methods of destroying
 CC chemical weapons and organophosphorous pesticides while avoiding the
 CC dangers inherent in burning these materials. It can be used in filtration
 CC equipment for individual soldiers and pesticide workers, and in vehicles,
 CC aircraft, ships and buildings such as civilian and military defence
 CC shelters, to perform detoxifications

XX

SQ Sequence 337 AA;

Query Match 99.8%; Score 1695; DB 5; Length 337;
 Best Local Similarity 99.7%; Pred. No. 1.1e-163;
 Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALA	EKA	VRGLR	60
Db	1	MSIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALA	EKA	VRGLR	60
Qy	61	RARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHIVAATGLWFDPP	LSMRLRS	VEELTQ	120
Db	61	RARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHIVAATGLWFDPP	LSMRLRS	VEELTQ	120
Qy	121	FFLREIQYGIEDTGIRAGIIKV	ATTGKATPFQELVLKAAARAS	LATGVPVT	THTAASQRD	180
Db	121	FFLREIQYGIEDTGIRAGIIKV	ATTGKATPFQELVLKAAARAS	LATGVPVT	THTAASQRD	180
Qy	181	GEQQAAIFESEGLSPSRVCIGH	SDDTDDL	SYLTALA	ARGYLIGLDH	IPHS
Db	181	GEQQAAIFESEGLSPSRVCIGH	SDDTDDL	SYLTALA	ARGYLIGLDH	IPHS
Qy	241	SALLGIRSWQTRALLIKALIDQ	GYMKQILV	SNDWLFG	FSSYVTN	IMDVMDRVNPDGMAFI
Db	241	SALLGIRSWQTRALLIKALIDQ	GYMKQILV	SNDWLFG	FSSYVTN	IMDVMDRVNPDGMAFI
Qy	301	PLRVIPFLREKGV	PQETLAGITVTN	PARFLSPTLRAS	337	
Db	301	PLRVIPFLREKGV	PQETLAGITVTN	PARFLSPTLRAS	337	

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	1688	99.4	365	2	Q8GC45	Q8gc45	flavobacter
2	1630	96.0	365	2	Q8VLR0	Q8vlr0	chryseobact
3	1558	91.8	384	2	Q93LD7	Q93ld7	agrobacteri
4	915	53.9	325	2	Q47934	Q47934	flavobacter
5	448	26.4	326	16	Q7U2I4	Q7u2i4	mycobacteri
6	408	24.0	314	17	Q97VT7	Q97vt7	sulfolobus
7	385	22.7	323	16	Q9RVU2	Q9rvu2	deinococcus
8	331	19.5	305	16	Q8Y5T5	Q8y5t5	listeria mo
9	325.5	19.2	362	16	Q985I1	Q985i1	rhizobium l
10	309	18.2	331	16	Q9KG87	Q9kg87	bacillus ha
11	306	18.0	292	16	Q8FCW5	Q8fcw5	escherichia
12	304	17.9	292	16	Q7UAS1	Q7uas1	shigella fl
13	296	17.4	679	16	Q9KF95	Q9kf95	bacillus ha
14	288	17.0	344	16	Q8FG90	Q8fg90	escherichia
15	277.5	16.3	355	16	Q8UBF0	Q8ubf0	agrobacteri
16	273	16.1	344	16	Q8XFU6	Q8xfu6	salmonella
17	270.5	15.9	349	13	Q7SZS2	Q7szs2	xenopus lae
18	269.5	15.9	330	16	Q8Y427	Q8y427	listeria mo
19	268.5	15.8	330	16	Q927J1	Q927j1	listeria in

RESULT 1

Q8GC45

ID Q8GC45 PRELIMINARY; PRT; 365 AA.
 AC Q8GC45;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Parathion hydrolase precursor (EC 3.1.8.1).
 GN OPD.
 OS Flavobacterium sp. ATCC 27551.
 OG Plasmid pPDL2.
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
 OC Flavobacteriaceae; Flavobacterium.
 OX NCBI_TaxID=74567;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27551;
 RA Siddavatam D., Manavathi B., Merrick M.;
 RT "The conserved region surrounding the organophosphorus pesticide
 RT degrading (opd) gene on the Flavobacterium plasmid pPDL2 has the
 RT features of a complex transposon.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ421424; CAD13181.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:0004063; F:aryldialkylphosphatase activity; IEA.
 DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0009056; P:catabolism; IEA.
 DR InterPro; IPR000437; Prok_lipoprot_S.
 DR InterPro; IPR001559; PTE.
 DR Pfam; PF02126; PTE; 1.
 DR PROSITE; PS01322; PHOSPHOTRIESTERASE_1; 1.
 DR PROSITE; PS01323; PHOSPHOTRIESTERASE_2; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Signal; Hydrolase; Plasmid.
 FT SIGNAL 1 29
 SQ SEQUENCE 365 AA; 38973 MW; 0C92FE577BFE4FB0 CRC64;

Query Match 99.4%; Score 1688; DB 2; Length 365;
 Best Local Similarity 99.7%; Pred. No. 8.6e-124;
 Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 61
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 Db 30 SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 89
 Qy 62 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF 121
 |||
 Db 90 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF 149
 Qy 122 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG 181
 |||
 Db 150 FLREIQYGIEDTGIRAGIIKVATTGKAAPFQELVLKAAARASLATGVPVTTHTAASQRDG 209
 Qy 182 EQQAAIFESEGLSPSRVCIGHSDDTDDLSTALAAARGYLIGLDHIPHSAIGLEDNASAS 241
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 Db 210 EQQAAIFESEGLSPSRVCIGHSDDTDDLSTALAAARGYLIGLDHIPHSAIGLEDNASAS 269

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Qy      242 ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP 301
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Db      270 ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP 329

Qy      302 LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 337
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Db      330 LRVIPFLREKGVQPQETLAGITVTNPARFLSPTLRAS 365

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RESULT 2

Q8VLR0

ID Q8VLR0 PRELIMINARY; PRT; 365 AA.

AC Q8VLR0;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Parathion hydrolase precursor (EC 3.1.8.1).

GN OPD.

OS Chryseobacterium balustinum.

OG Plasmid pBC9.

OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;

OC Flavobacteriaceae; Chryseobacterium.

OX NCBI_TaxID=246;

RN [1]

RP SEQUENCE FROM N.A.

RA Siddavatam D., Manavathi B., Merrick M.;

RT "The conserved region surrounding the organophosphorus pesticide

RT degrading (opd) gene on the Flavobacterium plasmid pPDL2 has the

RT features of a complex transposon.";

RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ426431; CAD19996.1; -.

DR GO; GO:0046821; C:extrachromosomal DNA; IEA.

DR GO; GO:0004063; F:aryldialkylphosphatase activity; IEA.

DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0009056; P:catabolism; IEA.

DR InterPro; IPR001559; PTE.

DR Pfam; PF02126; PTE; 1.

DR PROSITE; PS01322; PHOSPHOTRIESTERASE_1; 1.

DR PROSITE; PS01323; PHOSPHOTRIESTERASE_2; 1.

KW Signal; Hydrolase; Plasmid.

FT SIGNAL 1 29 POTENTIAL.

FT CHAIN 30 365 PARATHION HYDROLASE.

SQ SEQUENCE 365 AA; 39116 MW; AA9EC0E3BDD3F811 CRC64;

Query Match 96.0%; Score 1630; DB 2; Length 365;

Best Local Similarity 96.4%; Pred. No. 3e-119;

Matches 324; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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Qy      62 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHIVAATGLWFDPPPLSMRLRSVEELTQF 121
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Db      90 ARAAGVRTIVDVSTFDIGRDVSLLAEVSMVDSLLAETGLWFDPPPLSIGLRSVEELTQF 149
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Qy      122 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG 181
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Db      150 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG 209
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Qy      182 EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS 241
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Db      210 EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS 269
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Qy      242 ALLGIRSWQTRALLIKALIDQGYMKQILVSNWDLFGFSSYVTNIMDVMDRVNPDGMAFIP 301

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Db 270 |||||ALGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP 329

Qy 302 LRVIPFLREKGV PQETLAGITVTNPARFLSPTLRAS 337

Db 330 |||||LRVIPFLREKGV PQETLAGITVTNPARFLSPTLRAS 365

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query					
No.	Score	Match	Length	DB	ID		Description	
1	1689	99.5	336	4	US-09-603-450-4		Sequence 4, Appli	
2	1688	99.4	365	6	5484728-2		Patent No. 5484728	
3	267	15.7	352	4	US-09-543-681A-8100		Sequence 8100, Ap	
4	238.5	14.0	349	1	US-08-343-027A-12		Sequence 12, Appl	
5	105	6.2	477	4	US-09-489-039A-9937		Sequence 9937, Ap	
6	104	6.1	495	4	US-09-252-991A-21509		Sequence 21509, A	
7	99.5	5.9	2482	4	US-09-252-991A-16967		Sequence 16967, A	
8	92	5.4	908	4	US-09-328-352-7168		Sequence 7168, Ap	
9	91.5	5.4	461	4	US-09-134-000C-5551		Sequence 5551, Ap	
10	90.5	5.3	647	4	US-09-725-735A-18		Sequence 18, Appl	
11	90	5.3	569	4	US-09-543-681A-5106		Sequence 5106, Ap	
12	89.5	5.3	1161	4	US-09-252-991A-22872		Sequence 22872, A	
13	89	5.2	403	4	US-09-252-991A-25706		Sequence 25706, A	
14	89	5.2	655	4	US-09-107-532A-4425		Sequence 4425, Ap	
15	88.5	5.2	283	4	US-09-543-681A-8240		Sequence 8240, Ap	
16	87	5.1	288	4	US-09-252-991A-18721		Sequence 18721, A	
17	87	5.1	476	4	US-09-489-039A-14013		Sequence 14013, A	

RESULT 1

US-09-603-450-4

; Sequence 4, Application US/09603450

; Patent No. 6469145

; GENERAL INFORMATION:

; APPLICANT: Rastogi, Vipin K

; APPLICANT: Cheng, Tu-c

; APPLICANT: DeFrank, Joseph J

; TITLE OF INVENTION: One-Step Purification Process for Organophosphorus

; TITLE OF INVENTION: Hydrolase Enzyme

; FILE REFERENCE: DAM-508-99

; CURRENT APPLICATION NUMBER: US/09/603,450

; CURRENT FILING DATE: 2000-06-26

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 336

; TYPE: PRT

; ORGANISM: Flavobacterium sp

US-09-603-450-4

Query Match 99.5%; Score 1689; DB 4; Length 336;

Best Local Similarity 100.0%; Pred. No. 4.7e-174;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      2  IGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALA EKAVRGLRRA 61

Qy     63  RAAGVRTIVDVSTFDIGRDVSLLA EVSRAADVHI VAATGLWFD PPLSMRLRSVEELTQFF 122
          |||
Db     62  RAAGVRTIVDVSTFDIGRDVSLLA EVSRAADVHI VAATGLWFD PPLSMRLRSVEELTQFF 121

Qy    123  LREIQYGI EDTGIRAGI I KVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDGE 182
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Db    122  LREIQYGI EDTGIRAGI I KVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDGE 181

Qy    183  QQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHI PHSAIGLEDNASASA 242
          |||
Db    182  QQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHI PHSAIGLEDNASASA 241

Qy    243  LLGIRSWQTRALLIKALIDQGYMKQILVSN DWLFGFSSYVTNIMDVMDRVNPDGMAFIPL 302
          |||
Db    242  LLGIRSWQTRALLIKALIDQGYMKQILVSN DWLFGFSSYVTNIMDVMDRVNPDGMAFIPL 301

Qy    303  RVIPFLREKGV PQETLAGITVTNPARFLSPTLRAS 337
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Db    302  RVIPFLREKGV PQETLAGITVTNPARFLSPTLRAS 336

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Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	% Match				
1	1693	99.7	365	1	OPD_FLASP	P16648 flavobacter
2	448	26.4	326	1	PHP_MYCTU	P96413 mycobacteri
3	308	18.1	292	1	PHP_ECOLI	P45548 escherichia
4	243.5	14.3	349	1	PTER_HUMAN	Q96bw5 homo sapien
5	242.5	14.3	349	1	PTER_RAT	Q63530 rattus norv
6	239.5	14.1	349	1	PTER_MOUSE	Q60866 mus musculu
7	211.5	12.5	350	1	PTER_DROME	Q9vhf2 drosophila
8	127	7.5	216	1	YE97_MYCPN	P75290 mycoplasma
9	103	6.1	226	1	GPH2_PSEAE	Q9hz62 pseudomonas
10	103	6.1	319	1	HE31_STRCO	Q9wx16 streptomyce
11	96	5.7	342	1	ARGC_STRCO	P54895 streptomyce
12	93.5	5.5	352	1	TFTE_BURCE	Q45072 burkholderi
13	93	5.5	3421	1	TEGU_HSVEB	P28955 equine herp
14	92.5	5.4	522	1	LEU1_DEIRA	Q9rua9 deinococcus
15	92.5	5.4	898	1	SYA_METTH	O27718 methanobact
16	92	5.4	486	1	LE11_PYRAB	Q9uz08 pyrococcus
17	92	5.4	617	1	VATA_MANSE	P31400 manduca sex
18	91.5	5.4	494	1	TYRO_RHIME	P33180 rhizobium m
19	91.5	5.4	520	1	LEU1_YERPE	Q8zig8 yersinia pe
20	91.5	5.4	1139	1	VRNA_BSMV	P17595 barley stri
21	91	5.4	1290	1	RPOC_MYCPN	P75271 mycoplasma
22	90.5	5.3	333	1	YF72_HALN1	Q9hpl8 halobacteri
23	90.5	5.3	838	1	GLGB_STRAW	Q82jf0 streptomyce
24	89.5	5.3	300	1	Y505_MYCLE	Q49823 mycobacteri
25	89.5	5.3	308	1	Y505_MYCTU	Q11169 mycobacteri
26	89.5	5.3	435	1	PROA_BRAJA	Q89x85 bradyrhizob
27	89.5	5.3	958	1	GCP2_PSEAE	Q9htx7 pseudomonas
28	89	5.2	614	1	VAA2_DROME	Q27331 drosophila

RESULT 1

OPD_FLASP

ID OPD_FLASP STANDARD; PRT; 365 AA.
AC P16648; P13739;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Parathion hydrolase precursor (EC 3.1.8.1) (Phosphotriesterase)
DE (PTE).
GN OPD.
OS Flavobacterium sp. (strain ATCC 27551), and
OS Brevundimonas diminuta (Pseudomonas diminuta).
OG Plasmid pCMS1.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Flavobacterium.
OX NCBI_TaxID=239, 293;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-53.
RC SPECIES=Flavobacterium sp ATCC 27551;
RX MEDLINE=90078122; PubMed=2556372;
RA Mulbry W.W., Karns J.S.;
RT "Parathion hydrolase specified by the Flavobacterium opd gene:
RT relationship between the gene and protein.";
RL J. Bacteriol. 171:6740-6746(1989).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-44.
RC SPECIES=B.diminuta; STRAIN=MG;
RA Serdar C.M., Murdock D.C., Rohde M.F.;
RT "Parathion hydrolase gene from Pseudomonas diminuta MG: subcloning,
RT complete nucleotide sequence, and expression of the mature portion of
RT the enzyme in Escherichia coli.";
RL Biotechnology 7:1151-1155(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.diminuta; STRAIN=MG;
RX MEDLINE=88198028; PubMed=2834339;
RA McDaniel C.S., Harper L.L., Wild J.R.;
RT "Cloning and sequencing of a plasmid-borne gene (opd) encoding a
RT phosphotriesterase.";
RL J. Bacteriol. 170:2306-2311(1988).
RN [4]
RP ACTIVE SITE.
RX MEDLINE=94206935; PubMed=8155644;
RA Kuo J.M., Raushel F.M.;
RT "Identification of the histidine ligands to the binuclear metal
RT center of phosphotriesterase by site-directed mutagenesis.";
RL Biochemistry 33:4265-4272(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC SPECIES=B.diminuta;
RX MEDLINE=95092756; PubMed=7999757;
RA Benning M.M., Kuo J.M., Raushel F.M., Holden H.M.;
RT "Three-dimensional structure of phosphotriesterase: an enzyme capable
RT of detoxifying organophosphate nerve agents.";
RL Biochemistry 33:15001-15007(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RC SPECIES=B.diminuta;
 RX MEDLINE=95315185; PubMed=7794910;
 RA Benning M.M., Kuo J.M., Raushel F.M., Holden H.M.;
 RT "Three-dimensional structure of the binuclear metal center of
 RT phosphotriesterase.";
 RL Biochemistry 34:7973-7978(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RC SPECIES=B.diminuta;
 RX MEDLINE=96214508; PubMed=8634243;
 RA Vanhooke J.L., Benning M.M., Raushel F.M., Holden H.M.;
 RT "Three-dimensional structure of the zinc-containing
 RT phosphotriesterase with the bound substrate analog diethyl
 RT 4-methylbenzylphosphonate.";
 RL Biochemistry 35:6020-6025(1996).
 CC -!- FUNCTION: Has an unusual substrate specificity for synthetic
 CC organophosphate triesters and phosphorofluoridates. All of the
 CC phosphate triesters found to be substrates are synthetic
 CC compounds. The identity of any naturally occurring substrate for
 CC the enzyme is unknown. Has no detectable activity with phosphate
 CC monoesters or diesters and no activity as an esterase or protease.
 CC It catalyzes the hydrolysis of the insecticide paraoxon at a rate
 CC approaching the diffusion limit and thus appears to be optimally
 CC evolved for utilizing this synthetic substrate.
 CC -!- CATALYTIC ACTIVITY: Aryl dialkyl phosphate + H(2)O = dialkyl
 CC phosphate + an aryl alcohol.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit.
 CC -!- PATHWAY: Pesticide detoxification.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.
 CC -!- BIOTECHNOLOGY: Has attracted interest because of its potential use
 CC in the detoxification of chemical waste and warfare agents and its
 CC ability to degrade agricultural pesticides such as parathion.
 CC -!- SIMILARITY: Belongs to the phosphotriesterase family.
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to multiple
 CC sequencing errors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M29593; AAA24930.1; -.
 DR EMBL; M20392; AAA98299.1; ALT_FRAME.
 DR PIR; A28214; A28214.
 DR PIR; A43720; A43720.
 DR PDB; 1DPM; 20-AUG-97.
 DR PDB; 1EYW; 20-DEC-00.
 DR PDB; 1EZ2; 20-DEC-00.
 DR PDB; 1HZY; 04-APR-01.
 DR PDB; 1IOB; 04-APR-01.
 DR PDB; 1IOD; 04-APR-01.
 DR PDB; 1JGM; 04-JUL-01.
 DR PDB; 1PSC; 01-APR-97.

DR PDB; 1PTA; 01-DEC-95.
 DR InterPro; IPR000437; Prok_lipoprot_S.
 DR InterPro; IPR001559; PTE.
 DR Pfam; PF02126; PTE; 1.
 DR PROSITE; PS01322; PHOSPHOTRIESTERASE_1; 1.
 DR PROSITE; PS01323; PHOSPHOTRIESTERASE_2; 1.
 KW Hydrolase; Membrane; Plasmid; Signal; Metal-binding; Zinc;
 KW 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 365 PARATHION HYDROLASE.
 FT METAL 55 55 ZINC 1.
 FT METAL 57 57 ZINC 1.
 FT METAL 169 169 ZINC 1 AND 2.
 FT METAL 201 201 ZINC 2.
 FT METAL 230 230 ZINC 2.
 FT METAL 301 301 ZINC 1.
 FT STRAND 36 39
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 FT STRAND 249 252
 FT TURN 255 256
 FT TURN 260 261
 FT TURN 263 264

FT	HELIX	266	272
FT	HELIX	277	289
FT	TURN	290	291
FT	HELIX	293	295
FT	STRAND	296	298
FT	STRAND	305	306
FT	TURN	311	312
FT	HELIX	313	320
FT	TURN	322	323
FT	HELIX	324	326
FT	HELIX	327	330
FT	TURN	331	331
FT	HELIX	332	338
FT	TURN	339	340
FT	HELIX	343	350
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FT	HELIX	352	358
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Query Match 99.7%; Score 1693; DB 1; Length 365;
 Best Local Similarity 100.0%; Pred. No. 4.1e-128;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	SIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR	61
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Qy	62	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHI VAATGLWFDPP	121
Db	90	ARAAGVRTIVDVSTFDIGRDVSL	LAEVSRAADVHI VAATGLWFDPP	149
Qy	122	FLREIQYGI EDTGIRAGI I	KVATTGKATPFQELVLKAAARAS	181
Db	150	FLREIQYGI EDTGIRAGI I	KVATTGKATPFQELVLKAAARAS	209
Qy	182	EQQA AIFES EGLSPSRVCIGH	SDDTDDL SYLTALAARGYLIGLD	241
Db	210	EQQA AIFES EGLSPSRVCIGH	SDDTDDL SYLTALAARGYLIGLD	269
Qy	242	ALLGIRSWQTRALLI KALIDQ	GYMKQILVSN DWLFGFSSYVTN	301
Db	270	ALLGIRSWQTRALLI KALIDQ	GYMKQILVSN DWLFGFSSYVTN	329
Qy	302	LRVIPFLREKGV PQETLAGITV	TNPARFLSPTLRAS	337
Db	330	LRVIPFLREKGV PQETLAGITV	TNPARFLSPTLRAS	365